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1226-1
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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/529,043A

DATE: 08/29/2001

TIME: 15:22:39

Input Set : A:\21437.ST25.txt

Output Set: N:\CRF3\08292001\I529043A.raw

ENTERED

5 <110> APPLICANT: Eikmanns, Bernd
7 Peters-Wendisch, Petra
9 Sahm, Hermann
13 <120> TITLE OF INVENTION: METHOD FOR MICROBIAL PRODUCTION OF AMINO ACIDS OF THE
ASPARTATE

TECH CENTER 1600/2300

DEC 21 2001

RECT

14 AND/OR GLUTAMATE FAMILY

18 <130> FILE REFERENCE: 21437

22 <140> CURRENT APPLICATION NUMBER: 09/529,043A

24 <141> CURRENT FILING DATE: 2000-04-03

28 <160> NUMBER OF SEQ ID NOS: 2

32 <170> SOFTWARE: PatentIn version 3.0

36 <210> SEQ ID NO: 1

38 <211> LENGTH: 3728

40 <212> TYPE: DNA

42 <213> ORGANISM: Corynebacterium glutamicum

46 <400> SEQUENCE: 1

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51	ctatcaccct	tggcggcttc	ttgttgaaag	gaataattac	tctagtgtcg	actcacacat	180
53	cttcaacgct	tccagcattc	aaaaagatct	tggtagcaaa	ccgcggcgaa	atcgcggtcc	240
55	gtgctttccg	tgcagcactc	gaaaccggtg	cagccacggt	agctatttac	ccccgtgaag	300
57	atcggggatc	attccaccgc	tcttttgctt	ctgaagctgt	ccgcattggt	accgaaggct	360
59	caccagtcaa	ggcgtacctg	gacatcgatg	aaattatcgg	tgcagctaaa	aaagttaaag	420
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165 ctgcaacgaa ggtggaaggt ggcgacttga tcgtcgtcgt ttcctaaacc tttctgtaaa 3600
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176 <211> LENGTH: 1140
178 <212> TYPE: PRT
180 <213> ORGANISM: Corynebacterium glutamicum
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189 Val Ala Asn Arg Gly Glu Ile Ala Val Arg Ala Phe Arg Ala Ala Leu
190 20 25 30
192 Glu Thr Gly Ala Ala Thr Val Ala Ile Tyr Pro Arg Glu Asp Arg Gly
193 35 40 45
195 Ser Phe His Arg Ser Phe Ala Ser Glu Ala Val Arg Ile Gly Thr Glu
196 50 55 60
198 Gly Ser Pro Val Lys Ala Tyr Leu Asp Ile Asp Glu Ile Ile Gly Ala
199 65 70 75 80
201 Ala Lys Lys Val Lys Ala Asp Ala Ile Tyr Pro Gly Tyr Gly Phe Leu
202 85 90 95
204 Ser Glu Asn Ala Gln Leu Ala Arg Glu Cys Ala Glu Asn Gly Ile Thr

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205          100          105          110
207 Phe Ile Gly Pro Thr Pro Glu Val Leu Asp Leu Thr Gly Asp Lys Ser
208          115          120          125
210 Arg Ala Val Thr Ala Ala Lys Lys Ala Gly Leu Pro Val Leu Ala Glu
211          130          135          140
213 Ser Thr Pro Ser Lys Asn Ile Asp Glu Ile Val Lys Ser Ala Glu Gly
214 145          150          155          160
216 Gln Thr Tyr Pro Ile Phe Val Lys Ala Val Ala Gly Gly Gly Gly Arg
217          165          170          175
219 Gly Met Arg Phe Val Ala Ser Pro Asp Glu Leu Arg Lys Leu Ala Thr
220          180          185          190
222 Glu Ala Ser Arg Glu Ala Glu Ala Ala Phe Gly Asp Gly Ala Val Tyr
223          195          200          205
225 Val Glu Arg Ala Val Ile Asn Pro Gln His Ile Glu Val Gln Ile Leu
226          210          215          220
228 Gly Asp His Thr Gly Glu Val Val His Leu Tyr Glu Arg Asp Cys Ser
229 225          230          235          240
231 Leu Gln Arg Arg His Gln Lys Val Val Glu Ile Ala Pro Ala Gln His
232          245          250          255
234 Leu Asp Pro Glu Leu Arg Asp Arg Ile Cys Ala Asp Ala Val Lys Phe
235          260          265          270
237 Cys Arg Ser Ile Gly Tyr Gln Gly Ala Gly Thr Val Glu Phe Leu Val
238          275          280          285
240 Asp Glu Lys Gly Asn His Val Phe Ile Glu Met Asn Pro Arg Ile Gln
241          290          295          300
243 Val Glu His Thr Val Thr Glu Glu Val Thr Glu Val Asp Leu Val Lys
244 305          310          315          320
246 Ala Gln Met Arg Leu Ala Ala Gly Ala Thr Leu Lys Glu Leu Gly Leu
247          325          330          335
249 Thr Gln Asp Lys Ile Lys Thr His Gly Ala Ala Leu Gln Cys Arg Ile
250          340          345          350
252 Thr Thr Glu Asp Pro Asn Asn Gly Phe Arg Pro Asp Thr Gly Thr Ile
253          355          360          365
255 Thr Ala Tyr Arg Ser Pro Gly Gly Ala Gly Val Arg Leu Asp Gly Ala
256          370          375          380
258 Ala Gln Leu Gly Gly Glu Ile Thr Ala His Phe Asp Ser Met Leu Val
259 385          390          395          400
261 Lys Met Thr Cys Arg Gly Ser Asp Phe Glu Thr Ala Val Ala Arg Ala
262          405          410          415
264 Gln Arg Ala Leu Ala Glu Phe Thr Val Ser Gly Val Ala Thr Asn Ile
265          420          425          430
267 Gly Phe Leu Arg Ala Leu Leu Arg Glu Glu Asp Phe Thr Ser Lys Arg
268          435          440          445
270 Ile Ala Thr Gly Phe Ile Ala Asp His Pro His Leu Leu Gln Ala Pro
271          450          455          460
273 Pro Ala Asp Asp Glu Gln Gly Arg Ile Leu Asp Tyr Leu Ala Asp Val
274 465          470          475          480
276 Thr Val Asn Lys Pro His Gly Val Arg Pro Lys Asp Val Ala Ala Pro
277          485          490          495

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279 Ile Asp Lys Leu Pro Asn Ile Lys Asp Leu Pro Leu Pro Arg Gly Ser
280      500      505      510
282 Arg Asp Arg Leu Lys Gln Leu Gly Pro Ala Ala Phe Ala Arg Asp Leu
283      515      520      525
285 Arg Glu Gln Asp Ala Leu Ala Val Thr Asp Thr Thr Phe Arg Asp Ala
286      530      535      540
288 His Gln Ser Leu Leu Ala Thr Arg Val Arg Ser Phe Ala Leu Lys Pro
289 545      550      555      560
291 Ala Ala Glu Ala Val Ala Lys Leu Thr Pro Glu Leu Leu Ser Val Glu
292      565      570      575
294 Ala Trp Gly Gly Ala Thr Tyr Asp Val Ala Met Arg Phe Leu Phe Glu
295      580      585      590
297 Asp Pro Trp Asp Arg Leu Asp Glu Leu Arg Glu Ala Met Pro Asn Val
298      595      600      605
300 Asn Ile Gln Met Leu Leu Arg Gly Arg Asn Thr Val Gly Tyr Thr Pro
301      610      615      620
303 Tyr Pro Asp Ser Val Cys Arg Ala Phe Val Lys Glu Ala Ala Ser Ser
304 625      630      635      640
306 Gly Val Asp Ile Phe Arg Ile Phe Asp Ala Leu Asn Asp Val Ser Gln
307      645      650      655
309 Met Arg Pro Ala Ile Asp Ala Val Leu Glu Thr Asn Thr Ala Val Ala
310      660      665      670
312 Glu Val Ala Met Ala Tyr Ser Gly Asp Leu Ser Asp Pro Asn Glu Lys
313      675      680      685
315 Leu Tyr Thr Leu Asp Tyr Tyr Leu Lys Met Ala Glu Glu Ile Val Lys
316      690      695      700
318 Ser Gly Ala His Ile Leu Ala Ile Lys Asp Met Ala Gly Leu Leu Arg
319 705      710      715      720
321 Pro Ala Ala Val Thr Lys Leu Val Thr Ala Leu Arg Arg Glu Phe Asp
322      725      730      735
324 Leu Pro Val His Val His Thr His Asp Thr Ala Gly Gly Gln Leu Ala
325      740      745      750
327 Thr Tyr Phe Ala Ala Ala Gln Ala Gly Ala Asp Ala Val Asp Gly Ala
328      755      760      765
330 Ser Ala Pro Leu Ser Gly Thr Thr Ser Gln Pro Ser Leu Ser Ala Ile
331      770      775      780
333 Val Ala Ala Phe Ala His Thr Arg Arg Asp Thr Gly Leu Ser Leu Glu
334 785      790      795      800
336 Ala Val Ser Asp Leu Glu Pro Tyr Trp Glu Ala Val Arg Gly Leu Tyr
337      805      810      815
339 Leu Pro Phe Glu Ser Gly Thr Pro Gly Pro Thr Gly Arg Val Tyr Arg
340      820      825      830
342 His Glu Ile Pro Gly Gly Gln Leu Ser Asn Leu Arg Ala Gln Ala Thr
343      835      840      845
345 Ala Leu Gly Leu Ala Asp Arg Phe Glu Leu Ile Glu Asp Asn Tyr Ala
346      850      855      860
348 Ala Val Asn Glu Met Leu Gly Arg Pro Thr Lys Val Thr Pro Ser Ser
349 865      870      875      880
351 Lys Val Val Gly Asp Leu Ala Leu His Leu Val Gly Ala Gly Val Asp

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352		885		890		895
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355				900		
357	Val	Ile	Ala	Phe	Leu	Arg
358				915		
360	Pro	Glu	Pro	Leu	Arg	Thr
361				930		
363	Ala	Pro	Leu	Thr	Glu	Val
364	945			950		
366	Asp	Asp	Ser	Lys	Glu	Arg
367				965		
369	Lys	Pro	Thr	Glu	Glu	Phe
370				980		
372	Ser	Ala	Leu	Asp	Asp	Arg
373				995		
375	Glu	Thr	Leu	Ile	Arg	Leu
376				1010		
378	Arg	Leu	Asp	Ala	Ile	Ser
379				1025		
381	Val	Val	Ala	Asn	Val	Asn
382				1040		
384	Asp	Arg	Ser	Val	Glu	Ser
385				1055		
387	Ser	Ser	Asn	Lys	Gly	His
388				1070		
390	Thr	Val	Thr	Val	Ala	Glu
391				1085		
393	Val	Ala	Ile	Ile	Glu	Ala
394				1100		
396	Ser	Val	Asp	Gly	Lys	Ile
397				1115		
399	Lys	Val	Glu	Gly	Gly	Asp
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VERIFICATION SUMMARY

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